CRF Errors Corrected by the STIC Systems Branch

ENTERED

CRF Processing Date: 4/18/2001
Edited by: _____
Verified by: _____ AV (STIC staff)

Serial Number: 09/826,115

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentln bug). Sequences corrected: _____

☑ Other: *Sequence 7- corrected (222) responser* _____

_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 04/18/2001
PATENT APPLICATION: US/09/826,115   TIME: 16:42:46

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\04182001\I826115.raw**

Does Not Comply
Corrected Diskette Needed

```
   4 <110> APPLICANT: Chang, Gwong-Jen J
   6 <120> TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
   7       Flavivirus Infection
   9 <130> FILE REFERENCE: 14114.0332U3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/826,115
C--> 11 <141> CURRENT FILING DATE: 2001-04-04
  11 <150> PRIOR APPLICATION NUMBER: pct/us99/12298
  12 <151> PRIOR FILING DATE: 1999-06-03
  14 <150> PRIOR APPLICATION NUMBER: 09/701,536
  15 <151> PRIOR FILING DATE: 2000-11-29
  17 <150> PRIOR APPLICATION NUMBER: 60/087,908
  18 <151> PRIOR FILING DATE: 1998-06-04
  20 <160> NUMBER OF SEQ ID NOS: 31
  22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 48
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Artificial Sequence
  29 <220> FEATURE:
  30 <223> OTHER INFORMATION: Description of artificial sequence; note =
  31       synthetic construct
  33 <221> NAME/KEY: CDS
  34 <222> LOCATION: (25)...(48)
  36 <221> NAME/KEY: misc_feature
  37 <222> LOCATION: 1-48
  38 <223> OTHER INFORMATION: Amplimer 14DV389
  40 <400> SEQUENCE: 1
  41 cttggtacct ctagagccgc cgcc atg ggc aga aag caa aac aaa aga        48
  42                           Met Gly Arg Lys Gln Asn Lys Arg
  43                           1               5
  46 <210> SEQ ID NO: 2
  47 <211> LENGTH: 8
  48 <212> TYPE: PRT
  49 <213> ORGANISM: Artificial Sequence
  51 <220> FEATURE:
  52 <223> OTHER INFORMATION: Description of artificial sequence; note =
  53       synthetic construct
  55 <400> SEQUENCE: 2
  56 Met Gly Arg Lys Gln Asn Lys Arg
  57 1               5
  59 <210> SEQ ID NO: 3
  60 <211> LENGTH: 50
  61 <212> TYPE: DNA
  62 <213> ORGANISM: Artificial Sequence
  64 <220> FEATURE:
  65 <223> OTHER INFORMATION: Description of artificial sequence; note =
  66       synthetic construct
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RAW SEQUENCE LISTING   DATE: 04/18/2001
PATENT APPLICATION: US/09/826,115   TIME: 16:42:46

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 68 <221> NAME/KEY: misc_feature
 69 <222> LOCATION: 1-50
 70 <223> OTHER INFORMATION: Amplimer c14DV2453
 72 <400> SEQUENCE: 3
 73 ttttctttttg cggccgctca aacttaagca tgcacattgg tcgctaagaa          50
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 48
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Artificial Sequence
 80 <220> FEATURE:
 81 <223> OTHER INFORMATION: Description of artificial sequence; note =
 82       synthetic construct
 84 <221> NAME/KEY: CDS
 85 <222> LOCATION: (25)...(48)
 87 <221> NAME/KEY: misc_feature
 88 <222> LOCATION: (1)...(48)
 89 <223> OTHER INFORMATION: Amplimer YFDV389
 91 <400> SEQUENCE: 4
 92 cttggtacct ctagagccgc cgcc atg cgt tcc cat gat gtt ctg act       48
 93                           Met Arg Ser His Asp Val Leu Thr
 94                           1               5
 97 <210> SEQ ID NO: 5
 98 <211> LENGTH: 8
 99 <212> TYPE: PRT
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Description of artificial sequence; note =
104       synthetic construct
106 <400> SEQUENCE: 5
107 Met Arg Ser His Asp Val Leu Thr
108 1               5
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 41
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of artificial sequence; note =
117       synthetic construct
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: 1-41
121 <223> OTHER INFORMATION: Amplimer cYFDV2452
123 <400> SEQUENCE: 6
124 ttttctttttg cggccgctca cgccccaact cctagagaaa c                   41
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 51
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of artificial sequence; note =
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RAW SEQUENCE LISTING   DATE: 04/18/2001
PATENT APPLICATION: US/09/826,115   TIME: 16:42:46

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04182001\I826115.raw

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      133       synthetic construct
      135 <221> NAME/KEY: CDS
W-->  136 <222> LOCATION: (25)...(54)
      138 <221> NAME/KEY: misc_feature
W-->  139 <222> LOCATION: 1-51
      140 <223> OTHER INFORMATION: Amplimer SLEDV410
      142 <400> SEQUENCE: 7
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      144                           Met Ser Lys Lys Arg Gly Gly Thr Arg
      145                           1               5
      148 <210> SEQ ID NO: 8
      149 <211> LENGTH: 9
      150 <212> TYPE: PRT
      151 <213> ORGANISM: Artificial Sequence
      153 <220> FEATURE:
      154 <223> OTHER INFORMATION: Description of artificial sequence; note =
      155       synthetic construct
      157 <400> SEQUENCE: 8
      158 Met Ser Lys Lys Arg Gly Gly Thr Arg
      159 1               5
      161 <210> SEQ ID NO: 9
      162 <211> LENGTH: 38
      163 <212> TYPE: DNA
      164 <213> ORGANISM: Artificial Sequence
      166 <220> FEATURE:
      167 <223> OTHER INFORMATION: Description of artificial sequence; note =
      168       synthetic construct
      170 <221> NAME/KEY: misc_feature
      171 <222> LOCATION: 1-38
      172 <223> OTHER INFORMATION: Amplimer cSLEDV2449
      174 <400> SEQUENCE: 9
      175 ttttcttttg cggccgctta ggcttgcacg ctggttgc                            38
      177 <210> SEQ ID NO: 10
      178 <211> LENGTH: 7500
      179 <212> TYPE: DNA
      180 <213> ORGANISM: Artificial Sequence
      182 <220> FEATURE:
      183 <223> OTHER INFORMATION: Description of artificial sequence; note =
      184       synthetic construct
      186 <221> NAME/KEY: CDS
      187 <222> LOCATION: (916)...(3009)
      189 <221> NAME/KEY: misc_feature
      190 <222> LOCATION: 1-7500
      191 <223> OTHER INFORMATION: pCDJE 2-7
      193 <400> SEQUENCE: 10
      194 gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg      60
      195 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg     120
      196 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc     180
      197 ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt     240
```

```
198 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata   300
199 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   360
200 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc   420
201 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt   480
202 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt   540
203 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca   600
204 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg   660
205 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc   720
206 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg   780
207 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca   840
208 ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc   900
209 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa   951
210             Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
211               1                 5                  10
213 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg   999
214 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
215           15                  20                  25
217 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc   1047
218 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
219           30                  35                  40
221 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga   1095
222 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
223 45                  50                  55                  60
225 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag   1143
226 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
227                   65                  70                  75
229 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca   1191
230 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
231               80                  85                  90
233 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat   1239
234 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
235           95                  100                 105
237 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg   1287
238 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
239       110                 115                 120
241 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct   1335
242 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
243 125                 130                 135                 140
245 tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac   1383
246 Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
247               145                 150                 155
249 tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc   1431
250 Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
251               160                 165                 170
253 tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc   1479
254 Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
255           175                 180                 185
257 ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc   1527
258 Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
```

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259      190              195              200
261 aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg    1575
262 Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
263 205              210              215              220
265 gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca    1623
266 Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
267              225              230              235
269 aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag    1671
270 Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
271              240              245              250
273 gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg    1719
274 Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
275              255              260              265
277 gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat    1767
278 Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
279      270              275              280
281 agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac    1815
282 Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
283 285              290              295              300
285 gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc    1863
286 Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
287              305              310              315
289 tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc    1911
290 Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
291              320              325              330
293 aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac    1959
294 Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
295      335              340              345
297 cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt    2007
298 His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
299      350              355              360
301 aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac    2055
302 Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
303 365              370              375              380
305 gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa    2103
306 Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
307              385              390              395
309 gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg    2151
310 Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
311              400              405              410
313 gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca    2199
314 Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
315              415              420              425
317 gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc    2247
318 Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
319      430              435              440
321 aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat    2295
322 Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
323 445              450              455              460
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/826,115**

DATE: 04/18/2001
TIME: 16:42:47

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\04182001\I826115.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:136 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (25)...
(54)